

**b.) Amendments to the Claims:**

Applicants had previously submitted a Preliminary Amendment in the present application. In a telephone discussion with Examiner Borin on May 6, 2003, Applicants have learned that this amendment was never entered. A copy of the Preliminary Amendment is appended along with a copy of the return postcard evidencing the submission of the amendment. As per a telephone discussion with Examiner Borin on May 6, 2003, Applicants are proceeding as if the Preliminary Amendment were entered, and the changes made herein are being made with respect to the claims entered in that amendment. Accordingly, prior to this response claims 1-232 were pending. As of this amendment, claims 1-11, 16-37, and 64-232 are withdrawn from consideration. The following is a list of all claims that are pending in the application as of this office action, presented irrespective of whether the claim(s) remains under examination in the application. Status identifiers precede each claim.

1-11. (Withdrawn)

12. (Previously Amended) An enzyme having significant ~~(as herein defined)~~ sequence similarity to DAOCS, wherein the side chain binding site of ~~penicillin N~~ or DAOCS is modified and at least one amino acid residue and ~~at at least one~~ or more of the following sites ~~at least one amino acid residue~~ selected from the group consisting of Thr72, Arg74, Arg75, Glu156, Leu158, Arg160, Arg162, Leu186, Ser187, Phe225, Phe264, Arg266, Asp301, Tyr302, Val303, and Asn304; is changed to another amino acid residue or is deleted: ~~Thr72, Arg74, Arg75, Glu156, Leu158, Arg160, Arg162, Leu186, Ser187, Phe225, Phe264, Arg266, Asp301, Tyr302, Val303, and Asn304;~~ and/or ~~at least one additional amino acid residue is inserted within the region 300-311; provided that other residues interacting with the above may be changed in order to accommodate the change in one of the above.~~

13. (Previously Amended) An enzyme having significant ~~(as herein defined)~~ sequence similarity to DAOCS, wherein the penicillin/cephalosporin binding site of ~~penicillin N~~ or DAOCS is modified and ~~at at least one~~ or more of the following amino acid residues selected from the group consisting of Ile 88, Arg160, Arg162, Phe164, Met180, Thr190, Ile192, Phe225, Pro241, Val245, Val262, Phe264, Ile305, Arg 306, and Arg307; is changed

or deleted: [~~Ile 88, Arg160, Arg162, Phe164, Met180, Thr190, Ile192, Phe225, Pro241, Val245, Val262, Phe264, Ile305, Arg 306, and Arg307; and/or at least one additional amino acid residue is inserted within the region 300-311; provided that other residues interacting with the above may be changed in order to accommodate the change in one of the above~~].

14. (Previously Amended) An enzyme according to claim 12 ~~or claim 13~~ which is a mutant modification of DAOCS or DACS or DAOC/DACS.

15. (Previously Amended) An enzyme ~~as claimed in any one of claims 12-14~~ having significant sequence similarity to DAOCS, wherein both the side chain and the penicillin/cephalosporin binding sites of penicillin N or DAOC are modified and at least one of the residues ~~specified in claims 12 and 13~~ selected from the group consisting of Thr72, Arg74, Arg75, Ile88, Glu156, Leu158, Arg160, Arg162, Phe164, Met180, Leu186, Ser187, Thr190, Ile192, Phe225, Pro241, Val245, Val262, Phe264, Arg266, Asp301, Tyr302, Val303, Asn304; Ile305, Arg 306, and Arg307 is changed or deleted ~~and/or at least one additional amino acid residue is inserted within the region 300-311; provided that other residues interacting with the above may be changed in order to accommodate the change in one of the above~~.

16. -36. (Withdrawn).

37. (Previously Added) The enzyme of claim 12, further comprising the insertion of at least one additional amino acid residue within the region 300-311.

38. (Previously Added) An enzyme having significant sequence similarity to DAOCS, wherein the side chain binding site of DAOC is modified and at least one additional amino acid residue is inserted within the region 300-311.

39. (Previously Added) An enzyme having significant sequence similarity to DAOCS, wherein the side chain binding site of DAOC is modified and at least one amino acid residue at one or more of the following sites selected from the group consisting of Thr72, Arg74, Arg75, Glu156, Leu158, Arg160, Arg162, Leu186, Ser187, Phe225, Phe264, Arg266, Asp301, Tyr302, Val303, and Asn304; is changed to another amino acid residue or is deleted.

40. (Previously Added) The enzyme of claim 12, further comprising the insertion of at least one additional amino acid residue within the region 300-311.

41. (Previously Added) An enzyme having significant sequence similarity to DAOCS, wherein the side chain binding site of penicillin N is modified and at least one additional amino acid residue is inserted within the region 300-311.

42. (Previously Added) The enzyme of claim 13, further comprising the insertion of at least one additional amino acid residue within the region 300-311.

43. (Previously Added) An enzyme having significant sequence similarity to DAOCS, wherein the penicillin/cephalosporin binding site of DAOC is modified and at least one additional amino acid residue is inserted within the region 300-311.

44. (Previously Added) An enzyme having significant sequence similarity to DAOCS, wherein the penicillin/cephalosporin binding site of penicillin N is modified at one or more of the following amino acid residues selected from the group consisting of Ile 88, Arg160, Arg162, Phe164, Met180, Thr190, Ile192, Phe225, Pro241, Val245, Val262, Phe264, Ile305, Arg 306, and Arg307; is changed or deleted .

45. (Previously Added) The enzyme of claim 13, further comprising the insertion of at least one additional amino acid residue within the region 300-311.

46. (Previously Added) An enzyme having significant sequence similarity to DAOCS, wherein the penicillin/cephalosporin binding site of DAOC is modified and at least one additional amino acid residue is inserted within the region 300-311.

47. (Previously Added) The enzyme of claim 15, further comprising the insertion of at least one additional amino acid residue within the region 300-311.

48. (Previously Added) An enzyme having significant sequence similarity to DAOCS, wherein both side chain and the penicillin/cephalosporin binding site of DAOC are modified and at least one additional amino acid residue is inserted within the region 300-311.

49. (Previously Added) An enzyme according to claim 13 which is a modification of DAOCS or DACS or DAOC/DACS.

50. (Previously Added) An enzyme according to claim 15 which is a modification of DAOCS or DACS or DAOC/DACS.

51. (Previously Added) An enzyme as claimed in claim 13, wherein two or more complementary mutations are introduced to create or delete a binding interaction, including H-bonds, electrostatic, or hydrophobic interactions.

52. (Previously Added) An enzyme as claimed in claim 14, wherein two or more complementary mutations are introduced to create or delete a binding interaction, including H-bonds, electrostatic, or hydrophobic interactions.

53. (Previously Added) An enzyme as claimed in claim 49, wherein two or more complementary mutations are introduced to create or delete a binding interaction, including H-bonds, electrostatic, or hydrophobic interactions.

54. (Previously Added) An enzyme as claimed in claim 15, wherein two or more complementary mutations are introduced to create or delete a binding interaction, including H-bonds, electrostatic, or hydrophobic interactions.

55. (Previously Added) An enzyme as claimed in claim 37, wherein two or more complementary mutations are introduced to create or delete a binding interaction, including H-bonds, electrostatic, or hydrophobic interactions.

56. (Previously Added) An enzyme as claimed in claim 38, wherein two or more complementary mutations are introduced to create or delete a binding interaction, including H-bonds, electrostatic, or hydrophobic interactions.

57. (Previously Added) An enzyme as claimed in claim 39, wherein two or more complementary mutations are introduced to create or delete a binding interaction, including H-bonds, electrostatic, or hydrophobic interactions.

58. (Previously Added) An enzyme as claimed in claim 40, wherein two or more complementary mutations are introduced to create or delete a binding interaction, including H-bonds, electrostatic, or hydrophobic interactions.

59. (Previously Added) An enzyme as claimed in claim 41, wherein two or more complementary mutations are introduced to create or delete a binding interaction, including H-bonds, electrostatic, or hydrophobic interactions.

60. (Previously Added) An enzyme as claimed in claim 42, wherein two or more complementary mutations are introduced to create or delete a binding interaction, including H-bonds, electrostatic, or hydrophobic interactions.

61. (Previously Added) An enzyme as claimed in claim 43, wherein two or more complementary mutations are introduced to create or delete a binding interaction, including H-bonds, electrostatic, or hydrophobic interactions.

62. (Previously Added) An enzyme as claimed in claim 44, wherein two or more complementary mutations are introduced to create or delete a binding interaction, including H-bonds, electrostatic, or hydrophobic interactions.

63. (Previously Added) An enzyme as claimed in claim 45, wherein two or more complementary mutations are introduced to create or delete a binding interaction, including H-bonds, electrostatic, or hydrophobic interactions.

64. (Previously Added) An enzyme as claimed in claim 46, wherein two or more complementary mutations are introduced to create or delete a binding interaction, including H-bonds, electrostatic, or hydrophobic interactions.

65. (Previously Added) An enzyme as claimed in claim 47, wherein two or more complementary mutations are introduced to create or delete a binding interaction, including H-bonds, electrostatic, or hydrophobic interactions.

66 (Previously Added) An enzyme as claimed in claim 48, wherein two or more complementary mutations are introduced to create or delete a binding interaction, including H-bonds, electrostatic, or hydrophobic interactions.

67. -232. (Withdrawn)